Figure 1A

```
        10                  30                  50
GCGGGCTGCAGTCGCGGCGGCTTCTCCCCGCCTGGGCGGCCGCGCCGCTGGGCAGGTGCT
        70                  90                  110
GAGCGCCCCTAGAGCCTCCCTTGCCGCCTCCCTCCTCTGCCCGGCCGCAGCAGTGCACAT
       130                 150                 170
GGGGTGTTGGAGGTAGATGGGCTCCCGGCCCGGGAGGCGGCGGTGGATGCGGCGCTGGGC
       190                 210                 230
AGAAGCAGCCGCCGATTCCAGCTGCCCCGCGCGCCCCGGGCGCCCCTGCGAGTCCCCGGT
       250                 270                 290
TCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATCGCC
     M  G  T  S  P  S  S  S  T  A  L  A  S  C  S  R  I  A
       310                 330                 350
CGCCGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCTTAGCACC
R  R  A  T  A  T  M  I  A  G  S  L  L  L  L  G  F  L  S  T
       370                 390                 410
ACCACAGCTCAGCCAGAACAGAAGGCCTCGAATCTCATTGGCACATACCGCCATGTTGAC
T  T  A  Q  P  E  Q  K  A  S  N  L  I  G  T  Y  R  H  V  D
       430                 450                 470
CGTGCCACCGGCCAGGTGCTAACCTGTGACAAGTGTCCAGCAGGAACCTATGTCTCTGAG
R  A  T  G  Q  V  L  T  C  D  K  C  P  A  G  T  Y  V  S  E
       490                 510                 530
CATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCTGTGGGGACCTTTACCAGG
H  C  T  N  T  S  L  R  V  C  S  S  C  P  V  G  T  F  T  R
       550                 570                 590
CATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATGATT
H  E  N  G  I  E  K  C  H  D  C  S  Q  P  C  P  W  P  M  I
       610                 630                 650
GAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCCACCTGGCATGTTC
E  K  L  P  C  A  A  L  T  D  R  E  C  T  C  P  P  G  M  F
       670                 690                 710
CAGTCTAACGCTACCTGTGCCCCCCATACGGTGTGTCCTGTGGGTTGGGGTGTGCGGAAG
Q  S  N  A  T  C  A  P  H  T  V  C  P  V  G  W  G  V  R  K
       730                 750                 770
AAAGGGACAGAGACTGAGGATGTGCGGTGTAAGCAGTGTGCTCGGGGTACCTTCTCAGAT
K  G  T  E  T  E  D  V  R  C  K  Q  C  A  R  G  T  F  S  D
       790                 810                 830
GTGCCTTCTAGTGTGATGAAATGCAAAGCATACACAGACTGTCTGAGTCAGAACCTGGTG
V  P  S  S  V  M  K  C  K  A  Y  T  D  C  L  S  Q  N  L  V
       850                 870                 890
GTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCCTTCTCC
V  I  K  P  G  T  K  E  T  D  N  V  C  G  T  L  P  S  F  S
       910                 930                 950
AGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTTCCACGCCCTGAGCACATGGAAACC
S  S  T  S  P  S  P  G  T  A  I  F  P  R  P  E  H  M  E  T
       970                 990                1010
CATGAAGTCCCTTCCTCCACTTATGTTCCCAAAGGCATGAACTCAACAGAATCCAACTCT
H  E  V  P  S  S  T  Y  V  P  K  G  M  N  S  T  E  S  N  S
```

Figure 1B

```
      1030                 1050                 1070
TCTGCCTCTGTTAGACCAAAGGTACTGAGTAGCATCCAGGAAGGGACAGTCCCTGACAAC
S  A  S  V  R  P  K  V  L  S  S  I  Q  E  G  T  V  P  D  N
      1090                 1110                 1130
ACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTCCCAAACCTTCAGGTAGTC
T  S  S  A  R  G  K  E  D  V  N  K  T  L  P  N  L  Q  V  V
      1150                 1170                 1190
AACCACCAGCAAGGCCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAGGCC
N  H  Q  Q  G  P  H  H  R  H  I  L  K  L  L  P  S  M  E  A
      1210                 1230                 1250
ACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAG
T  G  G  E  K  S  S  T  P  I  K  G  P  K  R  G  H  P  R  Q
      1270                 1290                 1310
AACCTACACAAGCATTTTGACATCAATGAGCATTTGCCCTGGATGATTGTGCTTTTCCTG
N  L  H  K  H  F  D  I  N  E  H  L  P  W  M  I  V  L  F  L
      1330                 1350                 1370
CTGCTGGTGCTTGTGGTGATTGTGGTGTGCAGTATCCGGAAAAGCTCGAGGACTCTGAAA
L  L  V  L  V  V  I  V  V  C  S  I  R  K  S  S  R  T  L  K
      1390                 1410                 1430
AAGGGGCCCCGGCAGGATCCCAGTGCCATTGTGGAAAAGGCAGGGCTGAAGAAATCCATG
K  G  P  R  Q  D  P  S  A  I  V  E  K  A  G  L  K  K  S  M
      1450                 1470                 1490
ACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGATATC
T  P  T  Q  N  R  E  K  W  I  Y  Y  C  N  G  H  G  I  D  I
      1510                 1530                 1550
CTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAAGATATCTATCAGTTTCTTTGC
L  K  L  V  A  A  Q  V  G  S  Q  W  K  D  I  Y  Q  F  L  C
      1570                 1590                 1610
AATGCCAGTGAGAGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGG
N  A  S  E  R  E  V  A  A  F  S  N  G  Y  T  A  D  H  E  R
      1630                 1650                 1670
GCCTACGCAGCTCTGCAGCACTGGACCATCCGGGGCCCCGAGGCCAGCCTCGCCCAGCTA
A  Y  A  A  L  Q  H  W  T  I  R  G  P  E  A  S  L  A  Q  L
      1690                 1710                 1730
ATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAGAAGATTCGTGGGCTGATG
I  S  A  L  R  Q  H  R  R  N  D  V  V  E  K  I  R  G  L  M
      1750                 1770                 1790
GAAGACACCACCCAGCTGGAAACTGACAAACTAGCTCTCCCGATGAGCCCCAGCCCGCTT
E  D  T  T  Q  L  E  T  D  K  L  A  L  P  M  S  P  S  P  L
      1810                 1830                 1850
AGCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCCTGACGGTG
S  P  S  P  I  P  S  P  N  A  K  L  E  N  S  A  L  L  T  V
      1870                 1890                 1910
GAGCCTTCCCCACAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCTTCTC
E  P  S  P  Q  D  K  N  K  G  F  F  V  D  E  S  E  P  L  L
      1930                 1950                 1970
CGCTGTGACTCTACATCCAGCGGCTCCTCCGCGCTGAGCAGGAACGGTTCCTTTATTACC
R  C  D  S  T  S  S  G  S  S  A  L  S  R  N  G  S  F  I  T
```

Figure 1C

```
      1990                2010                2030
AAAGAAAAGAAGGACACAGTGTTGCGGCAGGTACGCCTGGACCCCTGTGACTTGCAGCCT
K  E  K  K  D  T  V  L  R  Q  V  R  L  D  P  C  D  L  Q  P
      2050                2070                2090
ATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAGATT
I  F  D  D  M  L  H  F  L  N  P  E  E  L  R  V  I  E  E  I
      2110                2130                2150
CCCCAGGCTGAGGACAAACTAGACCGGCTATTCGAAATTATTGGAGTCAAGAGCCAGGAA
P  Q  A  E  D  K  L  D  R  L  F  E  I  I  G  V  K  S  Q  E
      2170                2190                2210
GCCAGCCAGACCCTCCTGGACTCTGTTTATAGCCATCTTCCTGACCTGCTGTAGAACATA
A  S  Q  T  L  L  D  S  V  Y  S  H  L  P  D  L  L  *
      2230                2250                2270
GGGATACTGCATTCTGGAAATTACTCAATTTAGTGGCAGGGTGGTTTTTTAATTTTCTTC
      2290                2310                2330
TGTTTCTGATTTTTGTTGTTTGGGGTGTGTGTGTGTTTGTGTGTGTGTGTGTGTGTGT
      2350                2370                2390
GTGTGTGTGTGTGTGTGTGTTTAACAGAGAATATGGCCAGTGCTTGAGTTCTTTCTCC
      2410                2430                2450
TTCTCTCTCTCTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCC
      2470                2490                2510
AGGTGTAACTGTTGTGAAATACCCACCACTAAAGTTTTTTAAGTTCCATATTTTCTCCAT
      2530                2550                2570
TTTGCCTTCTTATGTATTTTCGAGATTATTCTGTGCACTTTAAATTTACTTAACTTACCA
      2590                2610                2630
TAAATGCAGTGTGACTTTTCCCACACACTGGATTGTGAGGCTCTTAACTTCTTAAAAGTA
      2650                2670                2690
TAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTCACACCTACTT
      2710                2730                2750
TTTAAAAACAAATATTATTACTATTTTTATTATTGTTTGTCCTTTATAAATTTTCTTAAA
      2770                2790                2810
GATTAAGAAAATTTAAGACCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCT
      2830                2850                2870
TTTAAATATGTCTTGTATAGTTCATATTCATGGCTGAAACTTGACCACACTATTGCTGAT
      2890                2910                2930
TGTATGGTTTTCACCTGGACACCGTGTAGAATGCTTGATTACTTGTACTCTTCTTATGCT
      2950                2970                2990
AATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGG
      3010                3030                3050
CTTGACAACTGGGCCACCAAAGAACTTGAACTTCACCTTTTAGGATTTGAGCTGTTCTGG
      3070                3090                3110
AACACATTGCTGCACTTTGGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAG
      3130                3150                3170
AATTTGCCCAGCTTTGCTTTAAAAGATGTCTTGTTTTTTATATACACATAATCAATAGGT
      3190                3210                3230
CCAATCTGCTCTCAAGGCCTTGGTCCTGGTGGGATTCCTTCACCAATTACTTTAATTAAA
      3250                3270                3290
AATGGCTGCAACTGTAAGAACCCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAA
```

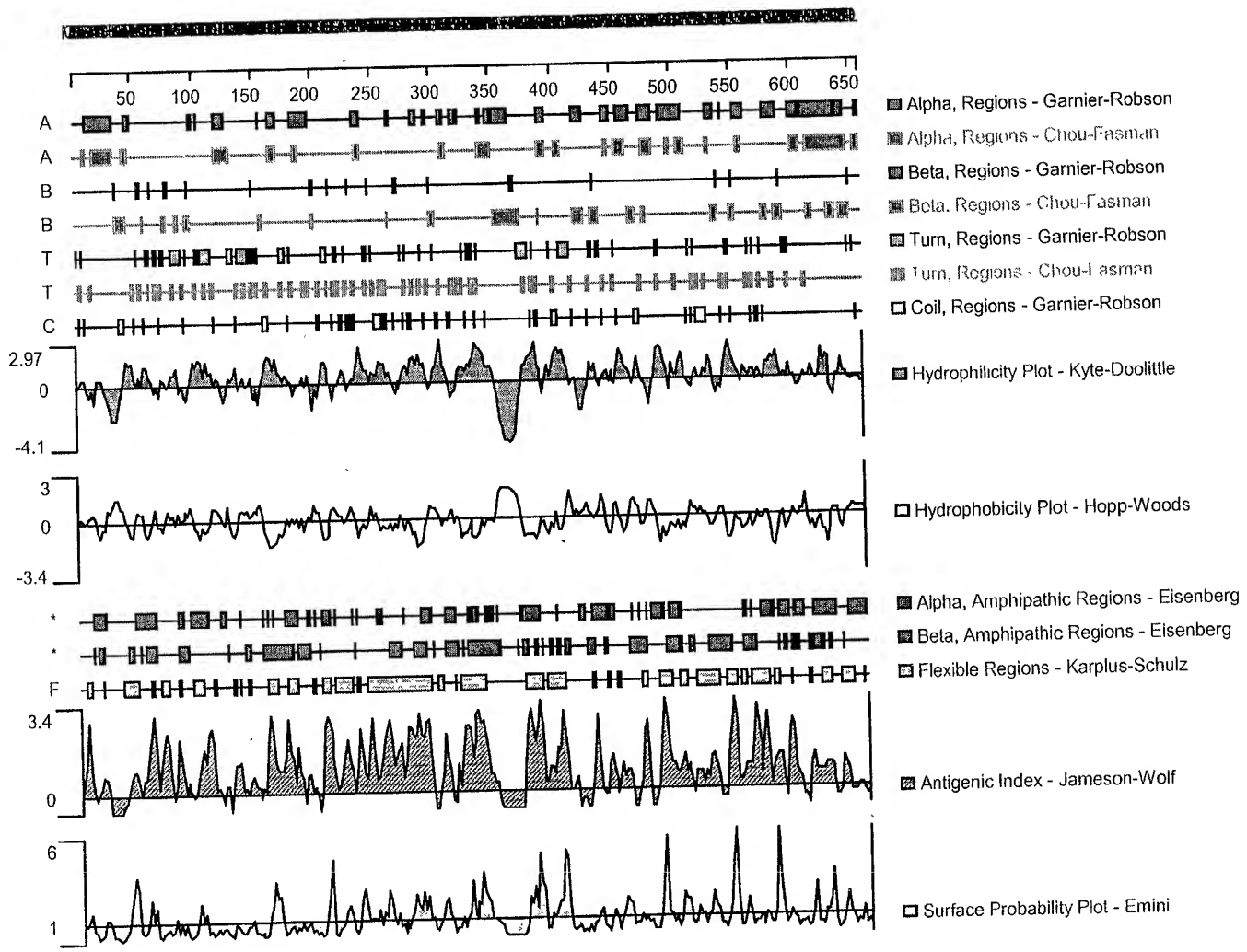
Figure 1D

```
      3310                 3330                 3350
ATGTACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTG
      3370                 3390                 3410
TGTGGGTGGGGTTTGTGGGTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGT
      3430                 3450                 3470
ACTAATTTATTAATAAACATTAGGTGTTTGTTAAAAAAAAAAAAAAAAAAAAAA
```

20070-426P1DOT

Figure 2

Figure 3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200
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650
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A
B
B
T
T
C
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Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.97
0
-4.1
Hydrophilicity Plot - Kyte-Doolittle
3
0
-3.4
Hydrophobicity Plot - Hopp-Woods
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini

Figure 4A

1 MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIGTYRHVDRATGQVLTCDKC 70
PAGTYVSEHCTNTSLRVCSSCPVGTFTRHENGIEKCHDCSQPCPWPMIEKLPCAALTDRECTCPPGMFQS 140
NATCAPHTVCPVGWGVRKKGTETEDVRCKQCARGTFSDVPSSVMKCKAYTDCLSQNLVVIKPGTKETDNV 210
CGTLPSFSSSTSPSPGTAIFPRPEHMETHEVPSSTYVPKGMNSTESNSSASVRPKVLSSIQEGTVPDNTS 280
SARGKEDVNKTLPNLQVVNHQQGPHHRHILKLLPSMEATGGEKSSTPIKGPKRGHPRQNLHKHFDINEHL 350
PWMIVLFLLLVLVVIVVCSIRKSSRTLKKGPRQDPSAIVEKAGLKKSMTPTQNREKWIYYCNGHGIDILK 420
LVAAQVGSQWKDIYQFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRRNDV 490
VEKIRGLMEDTTQLETDKLALPMSPSPLSPSPIPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLLRC 560
DSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQAEDKLDRLFE 630
IIGVKSQEASQTLLDSVYSHLPDLL 655

20070-4251A001

Figure 4B

```
T C D K C P A G T Y V S E H C T N T S L R V C S S C P V G T F T R H E N G I E K  TR9
L C D K C P P G T Y L K Q H C T A K W K T V C A P C P D H Y Y T D S W H T S D E  OPG

C H D C S Q P C P W P M I E K L P C A A L T D R E C T C P P G M F Q S N A T C A  TR9
C L Y C S P V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E F C L  OPG

P H T V C P V G W G V R K K G T E T E D V R C K Q C A R G T F S D V P S S V M K  TR9
K H R S C P P G F G V V Q A G T P E R N T V C K R C P D G F F S N E T S S K A P  OPG

                                                                              TR9
C K A Y T D C L S Q N L V V I K P G T K E T D N V C G                          OPG
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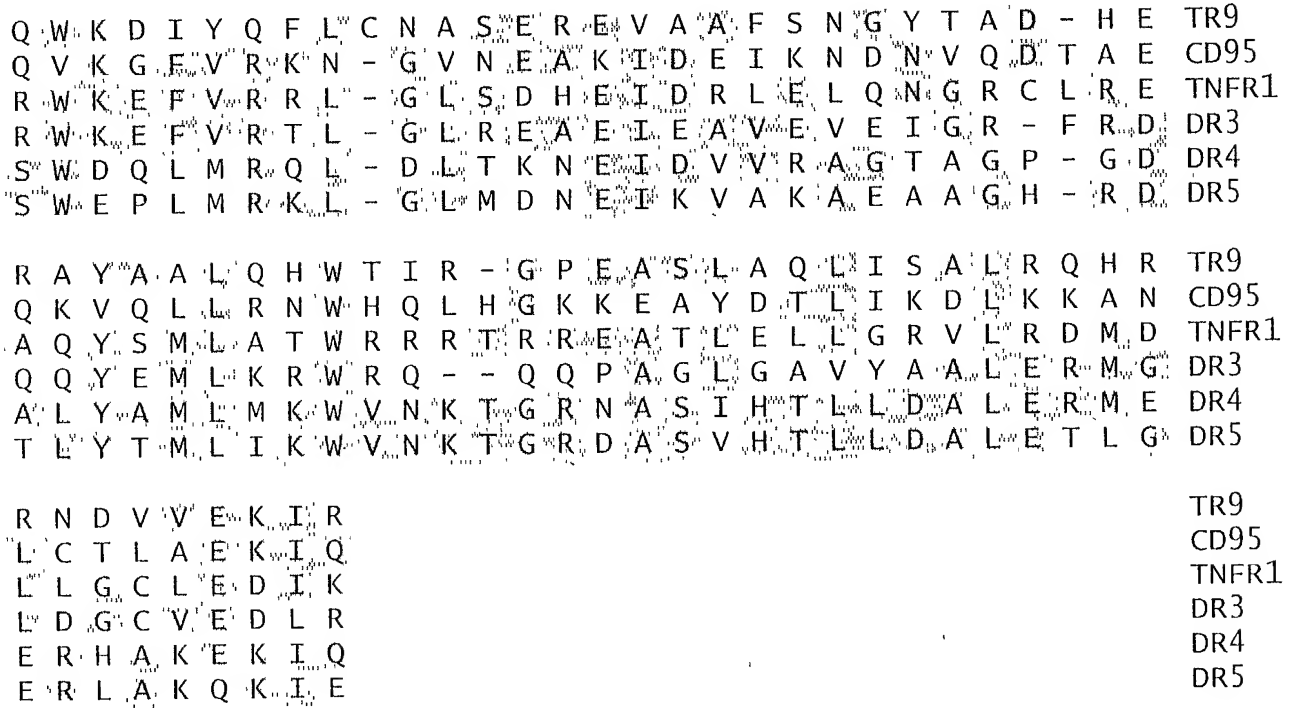
Figure 4C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S W E P L M R K L - G L M D N E I K V A K A E A A G H - R D DR5
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T L Y T M L I K W V N K T G R D A S V H T L L D A L E T L G DR5
R N D V V E K I R TR9
L C T L A E K I Q CD95
L L G C L E D I K TNFR1
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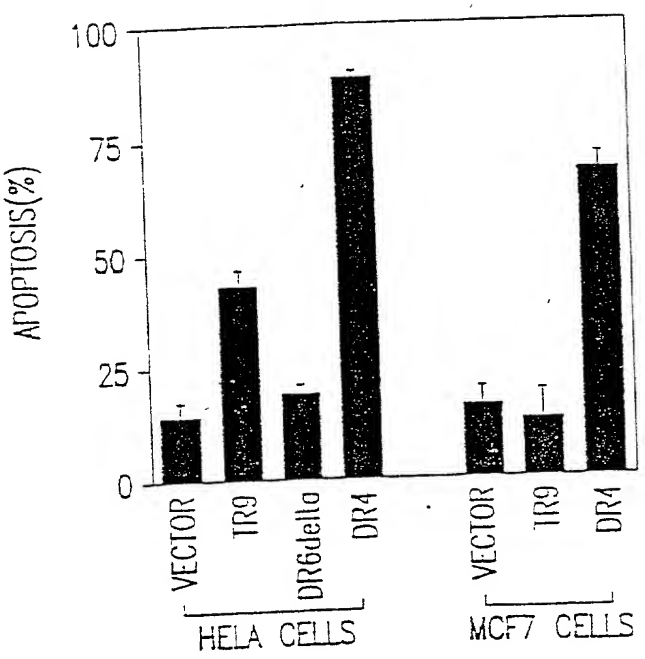
SUBSTITUTE SHEET (RULE 26)

Figure 5



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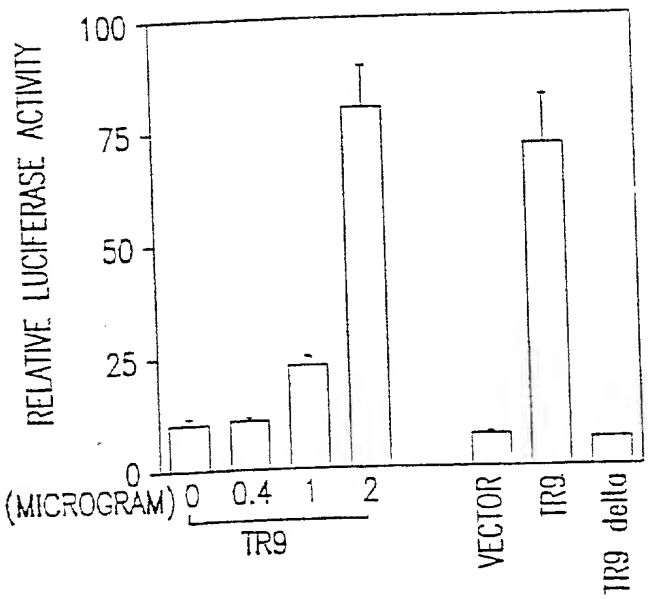
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